

Clone name	SEQ ID NO	Enantioselectivity for Neryl Butyrate (N) or Geranyl Butyrate (G)
1f15 (G2)	21	G
3C12	22	G
3N19 (G2)	23	G
G2.2	24	G
2C3	25	G
2F11	26	G
KV11 (6C7)	27	N
KV6 (3A1)	28	N
KV2 (2D1)	29	N
N2.5	30	N
KV5 (2H6)	31	N
3E5	32	G
G2.1	33	G
3H24 (G2)	34	G
KV10 (4G6)	35	N
KV12 (6D4)	36	N
N2.2	37	N
N2.3	38	N
N2.1	39	N
KV4 (2E12)	40	N
KV9 (4C6)	41	N
7D6	42	G
3F3	43	G
2D11 (G2)	44	G
3C23 (G2)	45	G
G2.3	46	G
2A3	47	G
2F4	48	G
2B9 (G2)	49	G
2C5	50	G
KV1 (2A6)	51	N
2D13 (G2)	52	G
3C8	53	G
2D5	54	G

FIGURE 1

Clone Name	E value for Neryl Butyrate	E value for Geranyl Butyrate
Exemplar (sgc2 and sgd2)	---	2.1
Exemplar (2h6)	1.4	---
Exemplar (14g14)	1.8	---
Exemplar (3f19a11)	2.2	(not tested)
Exemplar (3e5)	---	3.0
Exemplar (3n19)	---	3.8

FIGURE 2

09955066-071301

SEQ: 001-405 (pumilus)	(1)	-----ATGAAAATTGTAAAAAGAAAGGATCATTTGCA-----CTTGTAAACAATTTTGGTGTCTG--TCAGTCACATCGC	1
SEQ: 002-406 (subtilis)	(1)	-----ATGAAAATTGTAAAAAGAAAGGATCATTTGCA-----CTTGTAAACAATTTTGGTGTCTG--TCTGTTACATCGC	
SEQ: 003-402 (megat.)	(1)	-----ATGAAAATTGTAAAAAGAAAGGATCATTTGCA-----CTTGTAAACAATTTTGGTGTCTG--TCAGTCACATCGC	
SEQ: 004-400 (lentus)	(1)	-----ATGAAAATTGTAAAAAGAAAGGATCATTTGCA-----CTTGTAAACAATTTTGGTGTCTG--TCAGTCACATCGC	
SEQ: 005-396 (circul.)	(1)	-----ATGAAAATTGTAAAAAGAAAGGATCATTTGCA-----CTTGTAAACAATTTTGGTGTCTG--TCAGTCACATCGC	
SEQ: 006-392 (azotof.)	(1)	-----ATGAAAATTGTAAAAAGAAAGGATCATTTGCA-----CTTGTAAACAATTTTGGTGTCTG--TCAGTCACATCGC	
SEQ: 007-398 (firmus)	(1)	-----ATGAAAATTGTAAAAAGAAAGGATCATTTGCA-----CTTGTAAACAATTTTGGTGTCTG--TCAGTCACATCGC	
SEQ: 008-393 (badius)	(1)	-----ATGAAAATTGTAAAAAGAAAGGATCATTTGCA-----CTTGTAAACAATTTTGGTGTCTG--TCAGTCACATCGC	
SEQ: 009-Dc5h	(1)	-----ATGAAAATTGTAAAAAGAAAGGATCATTTGCA-----CTTGTAAACAATTTTGGTGTCTG--TCAGTCACATCGC	
SEQ: 010-Dc5f	(1)	-----ATGAAAATTGTAAAAAGAAAGGATCATTTGCA-----CTTGTAAACAATTTTGGTGTCTG--TCAGTCACATCGC	
SEQ: 011-Dc5c1	(1)	-----ATGAAAATTGTAAAAAGAAAGGATCATTTGCA-----CTTGTAAACAATTTTGGTGTCTG--TCAGTCACATCGC	
SEQ: 012-Dc5a2	(1)	-----ATGAAAATTGTAAAAAGAAAGGATCATTTGCA-----CTTGTAAACAATTTTGGTGTCTG--TCAGTCACATCGC	
SEQ: 013-Dc512	(1)	-----ATGAAAATTGTAAAAAGAAAGGATCATTTGCA-----CTTGTAAACAATTTTGGTGTCTG--TCAGTCACATCGC	
SEQ: 014-Sga	(1)	-----ATGAAAATTGTAAAAAGAAAGGATCATTTGCA-----CTTGTAAACAATTTTGGTGTCTG--TCAGTCACATCGC	
SEQ: 015-Sgc	(1)	-----ATGAAAATTGTAAAAAGAAAGGATCATTTGCA-----CTTGTAAACAATTTTGGTGTCTG--TCAGTCACATCGC	
SEQ: 016-Sgd	(1)	-----ATGAAAATTGTAAAAAGAAAGGATCATTTGCA-----CTTGTAAACAATTTTGGTGTCTG--TCAGTCACATCGC	
SEQ: 017-Sgf	(1)	-----ATGAAAATTGTAAAAAGAAAGGATCATTTGCA-----CTTGTAAACAATTTTGGTGTCTG--TCAGTCACATCGC	
SEQ: 018-Sgh	(1)	-----ATGAAAATTGTAAAAAGAAAGGATCATTTGCA-----CTTGTAAACAATTTTGGTGTCTG--TCAGTCACATCGC	
SEQ: 019-Mt2b1	(1)	-----ATGAAAATTGTAAAAAGAAAGGATCATTTGCA-----CTTGTAAACAATTTTGGTGTCTG--TCAGTCACATCGC	
SEQ: 020-H2a	(1)	-----ATGAAAATTGTAAAAAGAAAGGATCATTTGCA-----CTTGTAAACAATTTTGGTGTCTG--TCAGTCACATCGC	

Figure 3a

Figure 1 shows a vertical sequence of 12 micrographs illustrating the early development of a chick embryo. The stages are labeled as follows from top to bottom: 1. Fertilized egg, 2. 2-cell stage, 3. 4-cell stage, 4. 8-cell stage, 5. Morula stage, 6. Gastrula stage, 7. Somite stage, 8. Head stage, 9. Tail stage, 10. Hatching stage, 11. Hatched chick, and 12. Hatched chick. The images show the progression from a single cell to a fully formed chick.

	(Signal peptide coding region)	(Mature coding region)
SEQ: 001-405 (pumilus)	76	150
SEQ: 002-406 (subtilis)		
SEQ: 003-402 (megat.)		
SEQ: 004-400 (lentus)		
SEQ: 005-396 (circul.)		
SEQ: 006-392 (azotof.)		
SEQ: 007-398 (firmus)		
SEQ: 008-393 (badius)		
SEQ: 009-Dc5h		
SEQ: 010-Dc5f		
SEQ: 011-Dc5c1		
SEQ: 012-Dc5a2		
SEQ: 013-Dc512		
SEQ: 014-Sga		
SEQ: 015-Sgc		
SEQ: 016-Sgd		
SEQ: 017-Sgf		
SEQ: 018-Sgh		
SEQ: 019-Mt2b1		
SEQ: 020-H2a		

Figure 3b

151 225

SEQ: 001-405 (pumilus) (139) TCATACAAATTTTGC GGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCA CGGGGCAAGCTGTATGCGGTTGAT

SEQ: 002-406 (subtilis) (139) TCATTCAAATTTTGC GGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCA CGGGGCAAGCTGTATGCGGTTGAT

SEQ: 003-402 (megat.) (139) TCATACAAATTTTGC GGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCA CGGGGCAAGCTGTATGCGGTTGAT

SEQ: 004-400 (lentus) (139) TCATACAAATTTTGC GGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCA CGGGGCAAGCTGTATGCGGTTGAT

SEQ: 005-396 (circul.) (139) TCATACAAATTTTGC GGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCA CGGGGCAAGCTGTATGCGGTTGAT

SEQ: 006-392 (azotof.) (139) TCATACAAATTTTGC GGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCA CGGGGCAAGCTGTATGCGGTTGAT

SEQ: 007-398 (firmus) (139) TCATACAAATTTTGC GGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCA CGGGGCAAGCTGTATGCGGTTGAT

SEQ: 008-393 (badius) (139) TCATACAAATTTTGC GGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCA CGGGGCAAGCTGTATGCGGTTGAT

SEQ: 009-Dc5h (139) TCATACAAATTTTGC GGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCA CGGGGCAAGCTGTATGCGGTTGAT

SEQ: 010-Dc5f (139) TCATACAAATTTTGC GGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCA CGGGGCAAGCTGTATGCGGTTGAT

SEQ: 011-Dc5c1 (148) TCATACAAATTTTGC GGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCA CGGGGCAAGCTGTATGCGGTTGAT

SEQ: 012-Dc5a2 (148) TCATACAAATTTTGC GGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCA CGGGGCAAGCTGTATGCGGTTGAT

SEQ: 013-Dc512 (148) TCATACAAATTTTGC GGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCA CGGGGCAAGCTGTATGCGGTTGAT

SEQ: 014-Sga (139) TCATACAAATTTTGC GGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCA CGGGGCAAGCTGTATGCGGTTGAT

SEQ: 015-Sgc (139) TCATACAAATTTTGC GGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCA CGGGGCAAGCTGTATGCGGTTGAT

SEQ: 016-Sgd (139) TCATACAAATTTTGC GGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCA CGGGGCAAGCTGTATGCGGTTGAT

SEQ: 017-Sgf (139) TCATACAAATTTTGC GGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCA CGGGGCAAGCTGTATGCGGTTGAT

SEQ: 018-Sgh (139) TCATACAAATTTTGC GGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCA CGGGGCAAGCTGTATGCGGTTGAT

SEQ: 019-Mt2b1 (148) TCATACAAATTTTGC GGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCA CGGGGCAAGCTGTATGCGGTTGAT

SEQ: 020-H2a (139) TCATACAAATTTTGC GGGAATTAAGAGCTATCTCGTATCTCAGGGCTGGTCA CGGGGCAAGCTGTATGCGGTTGAT

Figure 3c

SEQ:001-405 (pumilus)	(214)	226	300
SEQ:002-406 (subtilis)	(214)	TTTTGGGACAAAGACAGGACGAAATTATAACAAATGATGACGATTTGTGCAAAAGGTTTGTAGACGAA	
SEQ:003-402 (megat.)	(214)	TTTTGGGACAAAGACAGGACGAAATTATAACAAATGATGACGATTTGTGCAAAAGGTTTGTAGACGAA	
SEQ:004-400 (lentus)	(214)	TTTTGGGACAAAGACAGGACGAAATTATAACAAATGATGACGATTTGTGCAAAAGGTTTGTAGACGAA	
SEQ:005-396 (circul.)	(214)	TTTTGGGACAAAGACAGGACGAAATTATAACAAATGATGACGATTTGTGCAAAAGGTTTGTAGACGAA	
SEQ:006-392 (azotof.)	(214)	TTTTGGGACAAAGACAGGACGAAATTATAACAAATGATGACGATTTGTGCAAAAGGTTTGTAGACGAA	
SEQ:007-398 (firmus)	(214)	TTTTGGGACAAAGACAGGACGAAATTATAACAAATGATGACGATTTGTGCAAAAGGTTTGTAGACGAA	
SEQ:008-393 (badius)	(214)	TTTTGGGACAAAGACAGGACGAAATTATAACAAATGATGACGATTTGTGCAAAAGGTTTGTAGACGAA	
SEQ:009-Dc5h	(214)	TTTTGGGACAAAGACAGGACGAAATTATAACAAATGATGACGATTTGTGCAAAAGGTTTGTAGACGAA	
SEQ:010-Dc5f	(214)	TTTTGGGACAAAGACAGGACGAAATTATAACAAATGATGACGATTTGTGCAAAAGGTTTGTAGACGAA	
SEQ:011-Dc5c1	(223)	TTCAAGGACAAAGACAGGACGAAATTATAACAAATGATGACGATTTGTGCAAAAGGTTTGTAGACGAA	
SEQ:012-Dc5a2	(223)	TTCTAAGACAAACAGGACGAAATTATAACAAATGATGACGATTTGTGCAAAAGGTTTGTAGACGAA	
SEQ:013-Dc512	(223)	TTCTAAGACAAACAGGACGAAATTATAACAAATGATGACGATTTGTGCAAAAGGTTTGTAGACGAA	
SEQ:014-Sga	(214)	TTCTAAGACAAACAGGACGAAATTATAACAAATGATGACGATTTGTGCAAAAGGTTTGTAGACGAA	
SEQ:015-Sgc	(214)	TTCTAAGACAAACAGGACGAAATTATAACAAATGATGACGATTTGTGCAAAAGGTTTGTAGACGAA	
SEQ:016-Sgd	(214)	TTCTAAGACAAACAGGACGAAATTATAACAAATGATGACGATTTGTGCAAAAGGTTTGTAGACGAA	
SEQ:017-Sgf	(214)	TTCTAAGACAAACAGGACGAAATTATAACAAATGATGACGATTTGTGCAAAAGGTTTGTAGACGAA	
SEQ:018-Sgh	(214)	TTCTAAGACAAACAGGACGAAATTATAACAAATGATGACGATTTGTGCAAAAGGTTTGTAGACGAA	
SEQ:019-Mt2b1	(223)	TTCTAAGACAAACAGGACGAAATTATAACAAATGATGACGATTTGTGCAAAAGGTTTGTAGACGAA	
SEQ:020-H2a	(214)	TTCTAAGACAAACAGGACGAAATTATAACAAATGATGACGATTTGTGCAAAAGGTTTGTAGACGAA	

Figure 3d

SEQ:001-405 (pumilus) (289) ACGGGTGCGAAAAAAGTGGATATTGTCGCTCACAGTATGGGTGGCGCGAAACACACACCTTACTACATAAAAAATCTG
 SEQ:002-406 (subtilis) (289) ACGGGTGCGAAAAAAGTGGATATTGTCGCTCACAGCATGGGGGCGCGAAACACACACTTTACTACATAAAAAATCTG
 SEQ:003-402 (megat.) (289) ACGGGTGCGAAAAAAGTGGATATTGTCGCTCACAGCATGGGTGGCGCGAAACACACACTTTACTACATAAAAAATCTG
 SEQ:004-400 (lentus) (289) ACGGGTGCGAAAAAAGTGGATATTGTCGCTCACAGCATGGGTGGCGCGAAACACACACTTTACTACATAAAAAATCTG
 SEQ:005-396 (circul.) (289) ACGGGTGCGAAAAAAGTGGATATTGTCGCTCACAGCATGGGTGGCGCGAAACACACACTTTACTACATAAAAAATCTG
 SEQ:006-392 (azotof.) (289) ACGGGTGCGAAAAAAGTGGATATTGTCGCTCACAGCATGGGTGGCGCGAAACACACACTTTACTACATAAAAAATCTG
 SEQ:007-398 (firmus) (289) ACGGGTGCGAAAAAAGTGGATATTGTCGCTCACAGCATGGGTGGCGCGAAACACACACTTTACTACATAAAAAATCTG
 SEQ:008-393 (badius) (289) ACGGGTGCGAAAAAAGTGGATATTGTCGCTCACAGCATGGGTGGCGCGAAACACACACTTTACTACATAAAAAATCTG
 SEQ:009-Dc5h (289) ACGGGTGCGAAAAAAGTGGATATTGTCGCTCACAGCATGGGTGGCGCGAAACACACACTTTACTACATAAAAAATCTG
 SEQ:010-Dc5f (289) ACGGGTGCGAAAAAAGTGGATATTGTCGCTCACAGCATGGGTGGCGCGAAACACACACTTTACTACATAAAAAATCTG
 SEQ:011-Dc5c1 (298) ACAGGTGCCAAAAAAGTGGATATTGTCGCTCACAGCATGGGTGGCGCGAAACACACACTTTACTACATAAAAAATCTG
 SEQ:012-Dc5a2 (298) ACAGGTGCCAAAAAAGTGGATATTGTCGCTCACAGCATGGGTGGCGCGAAACACACACTTTACTACATAAAAAATCTG
 SEQ:013-Dc512 (298) ACCGGTGCAGAAAAAAGTGGATATTGTCGCTCACAGCATGGGTGGCGCGAAACACACACTTTACTACATAAAAAATCTG
 SEQ:014-Sga (289) ACCGGTGCAGAAAAAAGTGGATATTGTCGCTCACAGCATGGGTGGCGCGAAACACACACTTTACTACATAAAAAATCTG
 SEQ:015-Sgc (289) ACCGGTGCAGAAAAAAGTGGATATTGTCGCTCACAGCATGGGTGGCGCGAAACACACACTTTACTACATAAAAAATCTG
 SEQ:016-Sgd (289) ACAGGAGCCAAAAAAGTGGATATTGTCGCTCACAGCATGGGTGGCGCGAAACACACACTTTACTACATAAAAAATCTG
 SEQ:017-Sgf (289) ACAGGAGCCAAAAAAGTGGATATTGTCGCTCACAGCATGGGTGGCGCGAAACACACACTTTACTACATAAAAAATCTG
 SEQ:018-Sgh (289) ACAGGAGCCAAAAAAGTGGATATTGTCGCTCACAGCATGGGTGGCGCGAAACACACACTTTACTACATAAAAAATCTG
 SEQ:019-Mt2b1 (298) ACAGGAGCCAAAAAAGTGGATATTGTCGCTCACAGCATGGGTGGCGCGAAACACACACTTTACTACATAAAAAATCTG
 SEQ:020-H2a (289) ACAGGAGCCAAAAAAGTGGATATTGTCGCTCACAGCATGGGTGGCGCGAAACACACACTTTACTACATAAAAAATCTG

Figure 3e

SEQ: 001-405 (pumilus) (364) GACGGCGGAAATAAAAATTGAAAACGTCGTAAACGCTTGGCGGCGGAAACCGTTTCAGCAGCAAGCAAGGCGCTTCCG
 SEQ: 002-406 (subtilis) (364) GACGGCGGAAATAAAGTTGAAAACGTCGTACGCTTGGCGGCGGAAACCGTTTGACGACAGCAAGGCGCTTCCG
 SEQ: 003-402 (megat.) (364) GACGGCGGAAATAAAAATTGAAAACGTCGTAAACGCTTGGCGGCGGAAACCGTTTGACGACAAAGGCGCTTCCG
 SEQ: 004-400 (lentus) (364) GACGGCGGAAATAAAAATTGAAAACGTCGTAAACGCTTGGCGGCGGAAACCGTTTGACGACAAAGGCGCTTCCG
 SEQ: 005-396 (circul.) (364) GACGGCGGAAATAAAAATTGAAAACGTCGTAAACGCTTGGCGGCGGAAACCGTTTGACGACAAAGGCGCTTCCG
 SEQ: 006-392 (azotof.) (364) GACGGCGGAAATAAAAATTGAAAACGTCGTAAACGCTTGGCGGCGGAAACCGTTTGACGACAAAGGCGCTTCCG
 SEQ: 007-398 (firmus) (364) GACGGCGGAAATAAAAATTGAAAACGTCGTAAACGCTTGGCGGCGGAAACCGTTTGACGACAAAGGCGCTTCCG
 SEQ: 008-393 (badius) (364) GACGGCGGAAATAAAAATTGAAAACGTCGTAAACGCTTGGCGGCGGAAACCGTTTGACGACAAAGGCGCTTCCG
 SEQ: 009-Dc5h (364) GATGGCGCGATATAAAATTGAGAAACGTTGTACAAATTGGTGGAGCAACCGGACTCGTTTCAAGCAGAGCATTACCA
 SEQ: 010-Dc5f (364) GACGTTGGAGATATAAAATTGAAAACGTCGTACATTAAGTGGAGCAACCGGACTCGTTATCATCTCAGAGCATTACCA
 SEQ: 011-Dc5c1 (373) GACGGCGCGATATAAAATAGAAAACGTTGTTACACTTGGTGGAGCAACCGGACTCGTTTTCATCTCAGAGCATTACCA
 SEQ: 012-Dc5a2 (373) GATGGCGCGATATAAATTGAGAAACGTTGTACAAATTGGTGGAGCAACCGGACTCGTTTCAAGCAGAGCATTACCA
 SEQ: 013-Dc512 (364) GATGGCGGTAATAAAATTGAAAACGTCGTAAACGCTTGGCGGCGGAAATCGTCTTGTGACAGGCAAGGCGCTTCCG
 SEQ: 014-Sga (364) GATGGCGGTAATAAAATTGAAAACGTCGTAAACGCTTGGCGGCGGAAATCGTCTTGTGACAGGCAAGGCGCTTCCG
 SEQ: 015-S9c (364) GATGGCGGTAATAAAATTGAAAACGTCGTAAACGCTTGGCGGCGGAAATCGTCTTGTGACAGGCAAGGCGCTTCCG
 SEQ: 016-S9d (364) GATGGCGGTAATAAAATTGAAAACGTCGTAAACGCTTGGCGGCGGAAATCGTCTTGTGACAGGCAAGGCGCTTCCG
 SEQ: 017-S9f (364) GATGGTGGCGATATAAAATTGAGAAACGTTGTACAAATTGGTGGAGCAACCGGACTCGTTTCAAGCAGAGCATTACCA
 SEQ: 018-S9h (364) GATGGTGGCGATATAAATTGAGAAACGTTGTACAAATTGGTGGAGCAACCGGACTCGTTTCAAGCAGAGCATTACCA
 SEQ: 019-Mt2b1 (373) GATGGCGGCGATATAAATTGAAAACGTCGTACCAATTGGTGGAGCAACCGGACTCGTTTTCATCTCAGAGCATTACCA
 SEQ: 020-H2a (364) GATGGCGGCGATATAAATTGAGAAACGTTGTACAAATTGGCGGAGCAACCGGACTCGTTTCAAGCAGAGCATTACCA

Figure 3f

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SEQ: 001-405 (pumilus) (439) GGAACAGATCCAAATCAAAAAGATTTTATACACATCCATTTACA - GCAGTGCCGATATGATGTGCATGAATTACTTT
 SEQ: 002-406 (subtilis) (439) GGAACAGATCCAAATCAAAAAGATTTTATACACATCCATTTACA - GCAGTGCCGATATGATGTGCATGAATTACTTT
 SEQ: 003-402 (megat.) (439) GGAACAGATCCAAATCAAAAAGATTTTATACACATCCATTTACA - GCAGTGCCGATATGATGTGCATGAATTACTTT
 SEQ: 004-400 (lentus) (439) GGAACAGATCCAAATCAAAAAGATTTTATACACATCCATTTACA - GCAGTGCCGATATGATGTGCATGAATTACTTT
 SEQ: 005-396 (circul.) (439) GGAACAGATCCAAATCAAAAAGATTTTATACACATCCATTTACA - GCAGTGCCGATATGATGTGCATGAATTACTTT
 SEQ: 006-392 (azotof.) (439) GGAACAGATCCAAATCAAAAAGATTTTATACACATCCATTTACA - GCAGTGCCGATATGATGTGCATGAATTACTTT
 SEQ: 007-398 (firmus) (439) GGAACAGATCCAAATCAAAAAGATTTTATACACATCCATTTACA - GCAGTGCCGATATGATGTGCATGAATTACTTT
 SEQ: 008-393 (badius) (439) GGAACAGATCCAAATCAAAAAGATTTTATACACATCCATTTACA - GCAGTGCCGATATGATGTGCATGAATTACTTT
 SEQ: 009-Dc5h (439) GGCACAGATCCAAATCAAAAAGATTTTATACACATCCATTTACA - GCAGTGCCGATATGATGTGCATGAATTACTTT
 SEQ: 010-Dc5f (439) GGCACAGATCCAAATCAAAAAGATTTTATACACATCCATTTACA - GCAGTGCCGATATGATGTGCATGAATTACTTT
 SEQ: 011-Dc5c1 (448) GGCACAGATCCAAATCAAAAAGATTTTATACACATCCATTTACA - GCAGTGCCGATATGATGTGCATGAATTACTTT
 SEQ: 012-Dc5a2 (448) GGCACAGATCCAAATCAAAAAGATTTTATACACATCCATTTACA - GCAGTGCCGATATGATGTGCATGAATTACTTT
 SEQ: 013-Dc512 (448) GGCACAGATCCAAATCAAAAAGATTTTATACACATCCATTTACA - GCAGTGCCGATATGATGTGCATGAATTACTTT
 SEQ: 014-Sga (439) GGCACAGATCCAAATCAAAAAGATTTTATACACATCCATTTACA - GCAGTGCCGATATGATGTGCATGAATTACTTT
 SEQ: 015-Sgc (439) GGCACAGATCCAAATCAAAAAGATTTTATACACATCCATTTACA - GCAGTGCCGATATGATGTGCATGAATTACTTT
 SEQ: 016-Sgd (439) GGCACAGATCCAAATCAAAAAGATTTTATACACATCCATTTACA - GCAGTGCCGATATGATGTGCATGAATTACTTT
 SEQ: 017-Sgf (439) GGCACAGATCCAAATCAAAAAGATTTTATACACATCCATTTACA - GCAGTGCCGATATGATGTGCATGAATTACTTT
 SEQ: 018-Sgh (439) GGCACAGATCCAAATCAAAAAGATTTTATACACATCCATTTACA - GCAGTGCCGATATGATGTGCATGAATTACTTT
 SEQ: 019-Mt2b1 (448) GGCACAGATCCAAATCAAAAAGATTTTATACACATCCATTTACA - GCAGTGCCGATATGATGTGCATGAATTACTTT
 SEQ: 020-H2a (439) GGCACAGATCCAAATCAAAAAGATTTTATACACATCCATTTACA - GCAGTGCCGATATGATGTGCATGAATTACTTT

Figure 39

SEQ: 001-405 (pumilus)	(513)	ATCAAAATTAGACGGT-GCTAAAAAC-GCTCAAATTCATGGCTTGGGCACATTGGTTATTATGATGAACAGCCAA
SEQ: 002-406 (subtilis)	(513)	ATCAAGATTAGATGGT-GCTAGAAAC-GTTCAAATTCATGGCGTTGGACACATCGGCCCTCTGTACAGCAGCCAA
SEQ: 003-402 (megat.)	(513)	ATCAAAATTAGACGGT-GCTAAAAAC-GTTCAAATTCATGGCGTTGGGCACATTGGTTATTGATGAACAGCCAA
SEQ: 004-400 (lentus)	(513)	ATCAAAATTAGACGGT-GCTAAAAAC-GTTCAAATTCATGGCGTTGGGCACATTGGTTATTGATGAACAGCCAA
SEQ: 005-396 (circul.)	(513)	ATCAAAATTAGACGGT-GCTAAAAAC-GTTCAAATTCATGGCGTTGGGCACATTGGTTATTGATGAACAGCCAA
SEQ: 006-392 (azotof.)	(513)	ATCAAAATTAGACGGT-GCTAAAAAC-GTACAAATTCATGGCGTTGGGCACATTGGTTATTGATGAACAGCCAA
SEQ: 007-398 (firmus)	(513)	ATCAAAATTAGACGGT-GCTAAAAAC-GTCAAATTCATGGCGTTGGGCACATTGGTTATTGATGAACAGCCAA
SEQ: 008-393 (badius)	(513)	ATCAAAATTAGACGGT-GCTAAAAAC-GTTCAAATTCATGGCGTTGGGCACATTGGCCCTCTGTACAGCAGCCAA
SEQ: 009-Dc5h	(513)	ATCAAGATTAGATGGT-GCGAGAAAC-GTTCAAATCCATGGCGTTGGACACATCGGCCCTCTGTACAGCAGCCAA
SEQ: 010-Dc5f	(513)	CTCTCGTTTAATTGGC-GCAAGAAAC-ATCCTGATCCATGGCGTTGGTCATATCGGCTCTATTAACTCAAGCCAA
SEQ: 011-Dc5c1	(522)	TTTCG-GTTTTAATTGGCGCAAGAAAC-GTCCCTGATCCACGGCGTTGGACATATCGGCTCTATTAACTCAAGCCAA
SEQ: 012-Dc5a2	(522)	CTCGC-GTTTTAATTGGCGCAAGAAAC-GTCCCTGATCCA-GGCGTTGGTCATATCGGCTCTATTAACTCAAGCCAA
SEQ: 013-Dc512	(522)	CTCTCAGTTTAATTGGCGCAAGAAAC-GTCCCTGATCCA-GGCGTTGGTCATATCGGCTCTATTAACTCAAGCCAA
SEQ: 014-Sga	(513)	AACAAAAATTAGACGGG-GCTAAAAAT-GTTCAAATTCATGGTGTGGACACATATCGGCCCTCTGTACAGCAGCCAA
SEQ: 015-Sgc	(513)	ATCAAAATTAGACGGG-GCTAAAAAT-GTTCAAATTCATGGTGTGGACACATATCGGCCCTCTGTACAGCAGCCAA
SEQ: 016-Sgd	(513)	ATCAAAATTAGACGGG-GCTAAAAAT-GTTCAAATTCATGGTGTGGACACATATCGGCCCTCTGTACAGCAGCCAA
SEQ: 017-Sgf	(513)	CTCTCGTTTAATTGGC-GCAAGAAAC-GTCCAAATCCATGGCGTTGGACATATCGGCCCTCTGTACAGCAGCCAA
SEQ: 018-Sgh	(513)	CTCTCGTTTAATTGGC-GCAAGAAAC-GTCCAAATCCATGGCGTTGGACATATCGGCCCTCTGTACAGCAGCCAA
SEQ: 019-mt2b1	(522)	TTTCG-GTTTTAATTGGC-GCAAGAAAC-GTCCCTGATCCACGGCGTTGGCCATATCGGCTCTATTAACTCAAGCCAA
SEQ: 020-H2a	(514)	CTCTCGTTTAATTGGCTGCAAGAAACAGTCCAAATTCATGGCGTTGGACATATCGGCTCTATTAACTCAAGCCAA

Figure 3h

SEQ:001-405 (pumilus)	(586)	601	GTCAACAGCCTGATTAAAGAAAGGACTGAACGGCGGGGGCCAAATAACGAATTAA
SEQ:002-406 (subtilis)	(586)		GTCAACAGCCTGATTAAAGAAAGGCTGAACGGCGGGGGACTCAATACAAATTAG
SEQ:003-402 (megat.)	(586)		GTCAACAGCCTGATTAAAGAAAGGACTGAACGGCGGGGGCCACAAATACAAATTAA
SEQ:004-400 (lentus)	(586)		GTCAACAGCCTGATTAAAGAAAGGACTGAACGGCGGGGGAGGACTAAATACAAATTAA
SEQ:005-396 (circul.)	(586)		GTCAACAGCCTGATTAAAGAAAGGACTGAACGGCGGGGGCTCAATACAAATTAA
SEQ:006-392 (azotof.)	(586)		GTCAACAGCCTGATTAAAGAAAGGACTGAACGGCGGGGGCTAGATACAAATTAA
SEQ:007-398 (firmus)	(586)		GTCAACAGCCTGATTAAAGAAAGGACTGAACGGCGGGGGCCACAAATACAAATTAA
SEQ:008-393 (badius)	(586)		GTCAACAGCCTGATTAAAGAAAGGCTGAACGGCGGGGGCTCAATACAAATTAA
SEQ:009-Dc5h	(586)		GTGAAAGGGTATTAAAGAAAGGACTGAACGGCGGGGGCTCAATACAAATTAA
SEQ:010-Dc5f	(586)		GTCAAAGGCTATTGAAAGAAAGGACTGAATGGCGGGGGACAGAATACAAATTAA
SEQ:011-Dc5c1	(595)		GTCAAAGGCTATATCAAAGAAAGGACTGAATGGCGGGGGACAGCCAAATACAAATTAA
SEQ:012-Dc5a2	(595)		GTGAAAGGGTATTAAAGAAAGGACTGAACGGCGGGGGCTCAATACAAATTAA
SEQ:013-Dc512	(595)		GTCAACAGCCTGATTAAAGAAAGGCTTAACGGCGGGAGGCTCAATACAAATTAA
SEQ:014-Sga	(586)		GTCAATAGCCTGATTAAAGAAAGGCTTAACGGCGGGAGGACTCAATACGAATTAA
SEQ:015-Sgc	(586)		GTCAACAGCCTGATTAAAGAAAGGCTTAACGGCGGGGGCTGAATACGAATTAA
SEQ:016-Sgd	(586)		GTCAAGGATATATTAAAGAAAGGACTGAACGGCGGGGGCTCAATACAAATTAA
SEQ:017-Sgf	(586)		GTCAAGGATATATTAAAGAAAGGACTGAACGGCGGGGGCTCAATACAAATTAA
SEQ:018-Sgh	(586)		GTGAAAGGGTATTAAAGAAAGGACTGAACGGCGGGGGCTAAATACAAATTAA
SEQ:019-Mt2b1	(595)		GTCAAAGGATATATTAAAGAAAGGACTGAACGGCGGGGGCTAAATACAAATTAA
SEQ:020-H2a	(589)		

Figure 3i

SEQ: 021-1 f15 (G2)	1	TGAAACACAAATCCAGTTGTTATGGTTACCGTATTTGAGGGGCATCATTCAAATTTTTCGGGAAATTAAGAGCTATCT
SEQ: 022-3C12	(1)	TGAAACACAAATCCAGTTGTTATGGTTACCGTATTTGAGGGGCATCATTCAAATTTTTCGGGAAATTAAGAGCTATCT
SEQ: 023--3N19 (G2)	(1)	TGAAACACAAATCCAGTTGTTATGGTTACCGTATTTGAGGGGCATCATTCAAATTTTTCGGGAAATTAAGAGCTATCT
SEQ: 024-G2.2	(1)	TGAAACACAAATCCAGTTGTTATGGTTACCGTATTTGAGGGGCATCATTCAAATTTTTCGGGAAATTAAGAGCTATCT
SEQ: 025-2C3	(1)	TGAAACACAAATCCAGTTGTTATGGTTACCGTATTTGAGGGGCATCATTCAAATTTTTCGGGAAATTAAGAGCTATCT
SEQ: 026-2F11	(1)	TGAAACACAAATCCAGTTGTTATGGTTACCGTATTTGAGGGGCATCATTCAGTTTTTTCGGGAAATTAAGAGCTATCT
SEQ: 027-KV11 (6C7)	(1)	TGAAACACAAATCCAGTTGTTATGGTTACCGTATTTGAGGGGCATCATTCAGTTTTTTCGGGAAATTAAGAGCTATCT
SEQ: 028-KV6 (3A1)	(1)	TGAAACACAAATCCAGTTGTTATGGTTACCGTATTTGAGGGGCATCATTCAGTTTTTTCGGGAAATTAAGAGCTATCT
SEQ: 029-KV2 (2D1)	(1)	TGAAACACAAATCCAGTTGTTATGGTTACCGTATTTGAGGGGCATCATTCAGTTTTTTCGGGAAATTAAGAGCTATCT
SEQ: 030-N2.5	(1)	TGAAACACAAATCCAGTTGTTATGGTTACCGTATTTGAGGGGCATCATTCAGTTTTTTCGGGAAATTAAGAGCTATCT
SEQ: 031-KV5 (2H6)	(1)	TGAAACACAAATCCAGTTGTTATGGTTACCGTATTTGAGGGGCATCATTCAGTTTTTTCGGGAAATTAAGAGCTATCT
SEQ: 032-3E5	(1)	TGAAACACAAATCCAGTTGTTATGGTTACCGTATTTGAGGGGCATCATTCAGTTTTTTCGGGAAATTAAGAGCTATCT
SEQ: 033-G2.1	(1)	TGAAACACAAATCCAGTTGTTATGGTTACCGTATTTGAGGGGCATCATTCAGTTTTTTCGGGAAATTAAGAGCTATCT
SEQ: 034-3H24 (G2)	(1)	TGAAACACAAATCCAGTTGTTATGGTTACCGTATTTGAGGGGCATCATTCAGTTTTTTCGGGAAATTAAGAGCTATCT
SEQ: 035-KV10 (4G6)	(1)	TGAAACACAAATCCAGTTGTTATGGTTACCGTATTTGAGGGGCATCATTCAGTTTTTTCGGGAAATTAAGAGCTATCT
SEQ: 036-KV12 (6D4)	(1)	TGAAACACAAATCCAGTTGTTATGGTTACCGTATTTGAGGGGCATCATTCAGTTTTTTCGGGAAATTAAGAGCTATCT
SEQ: 037-N2.2	(1)	TGAAACACAAATCCAGTTGTTATGGTTACCGTATTTGAGGGGCATCATTCAGTTTTTTCGGGAAATTAAGAGCTATCT
SEQ: 038-N2.3	(1)	TGAAACACAAATCCAGTTGTTATGGTTACCGTATTTGAGGGGCATCATTCAGTTTTTTCGGGAAATTAAGAGCTATCT
SEQ: 039-N2.1	(1)	TGAAACACAAATCCAGTTGTTATGGTTACCGTATTTGAGGGGCATCATTCAGTTTTTTCGGGAAATTAAGAGCTATCT
SEQ: 040-KV4 (2E12)	(1)	TGAAACACAAATCCAGTTGTTATGGTTACCGTATTTGAGGGGCATCATTCAGTTTTTTCGGGAAATTAAGAGCTATCT
SEQ: 041-KV9 (4C6)	(1)	TGAAACACAAATCCAGTTGTTATGGTTACCGTATTTGAGGGGCATCATTCAGTTTTTTCGGGAAATTAAGAGCTATCT
SEQ: 042-7D6	(1)	TGAAACACAAATCCAGTTGTTATGGTTACCGTATTTGAGGGGCATCATTCAGTTTTTTCGGGAAATTAAGAGCTATCT
SEQ: 043-3F3	(1)	TGAAACACAAATCCAGTTGTTATGGTTACCGTATTTGAGGGGCATCATTCAGTTTTTTCGGGAAATTAAGAGCTATCT
SEQ: 044-2D11 (G2)	(1)	TGAAACACAAATCCAGTTGTTATGGTTACCGTATTTGAGGGGCATCATTCAGTTTTTTCGGGAAATTAAGAGCTATCT
SEQ: 045-3C23 (G2)	(1)	TGAAACACAAATCCAGTTGTTATGGTTACCGTATTTGAGGGGCATCATTCAGTTTTTTCGGGAAATTAAGAGCTATCT
SEQ: 046-G2.3	(1)	TGAAACACAAATCCAGTTGTTATGGTTACCGTATTTGAGGGGCATCATTCAGTTTTTTCGGGAAATTAAGAGCTATCT
SEQ: 047-2A3	(1)	TGAAACACAAATCCAGTTGTTATGGTTACCGTATTTGAGGGGCATCATTCAGTTTTTTCGGGAAATTAAGAGCTATCT
SEQ: 048-2F4	(1)	TGAAACACAAATCCAGTTGTTATGGTTACCGTATTTGAGGGGCATCATTCAGTTTTTTCGGGAAATTAAGAGCTATCT
SEQ: 049-2B9 (G2)	(1)	TGAAACACAAATCCAGTTGTTATGGTTACCGTATTTGAGGGGCATCATTCAGTTTTTTCGGGAAATTAAGAGCTATCT
SEQ: 050-2C5	(1)	TGAAACACAAATCCAGTTGTTATGGTTACCGTATTTGAGGGGCATCATTCAGTTTTTTCGGGAAATTAAGAGCTATCT
SEQ: 051-KV1 (2A6)	(1)	TGAAACACAAATCCAGTTGTTATGGTTACCGTATTTGAGGGGCATCATTCAGTTTTTTCGGGAAATTAAGAGCTATCT
SEQ: 052-2D13 (G2)	(1)	TGAAACACAAATCCAGTTGTTATGGTTACCGTATTTGAGGGGCATCATTCAGTTTTTTCGGGAAATTAAGAGCTATCT
SEQ: 053-3C8	(1)	TGAAACACAAATCCAGTTGTTATGGTTACCGTATTTGAGGGGCATCATTCAGTTTTTTCGGGAAATTAAGAGCTATCT
SEQ: 054-2D5	(1)	TGAAACACAAATCCAGTTGTTATGGTTACCGTATTTGAGGGGCATCATTCAGTTTTTTCGGGAAATTAAGAGCTATCT

Figure 4a

SEQ: 021-1f15 (G2) (76) CGTATCTCAGGGCTGGTCGCGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA
SEQ: 022-3C12 (76) CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA
SEQ: 023-3N19 (G2) (76) CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA
SEQ: 024-G2.2 (76) CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA
SEQ: 025-2C3 (76) CGTATCTCAGGGCTGGTCGCGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA
SEQ: 026-2F11 (76) CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA
SEQ: 027-KV11 (6C7) (76) CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA
SEQ: 028-KV6 (3A1) (76) CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA
SEQ: 029-KV2 (2D1) (76) CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA
SEQ: 030-N2.5 (76) CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA
SEQ: 031-KV5 (2H6) (76) CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA
SEQ: 032-3E5 (76) CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA
SEQ: 033-G2.1 (76) CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA
SEQ: 034-3H24 (G2) (76) CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA
SEQ: 035-KV10 (4G6) (76) CGTATCTCAGGGCTGGTCGCGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA
SEQ: 036-KV12 (6D4) (76) CGTATCTCAGGGCTGGTCGCGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA
SEQ: 037-N2.2 (76) CGTATCTCAGGGCTGGTCGCGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA
SEQ: 038-N2.3 (76) CGTATCTCAGGGCTGGTCGCGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA
SEQ: 039-N2.1 (76) CGTATCTCAGGGCTGGTCGCGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA
SEQ: 040-KV4 (2E12) (76) CGTATCTCAGGGCTGGTCACGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA
SEQ: 041-KV9 (4C6) (76) CGTATCTCAGGGCTGGTCGCGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA
SEQ: 042-7D6 (76) CGTATCTCAGGGCTGGTCGCGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA
SEQ: 043-3F3 (76) CGTATCTCAGGGCTGGTCGCGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA
SEQ: 044-2D11 (G2) (76) CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA
SEQ: 045-3C23 (G2) (76) CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA
SEQ: 046-G2.3 (76) CGTATCTCAGGGCTGGTCGCGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA
SEQ: 047-2A3 (76) CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA
SEQ: 048-2F4 (76) CGTATCTCAGGGCTGGTCGCGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA
SEQ: 049-2B9 (G2) (76) CGTATCTCAGGGCTGGTCGCGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA
SEQ: 050-2C5 (76) CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA
SEQ: 051-KV1 (2A6) (76) CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA
SEQ: 052-2D13 (G2) (76) CGTATCTCAGGGCTGGTCGCGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA
SEQ: 053-3C8 (76) CGTATCTCAGGGCTGGTCGCGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA
SEQ: 054-2D5 (76) CGTATCTCAGGGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTGGGACAAGACAGGGACGAAATTATAACAA

Figure 4b

SEQ: 021-1f15 (G2) (151) TGGCCCGGTATTATCGCGTTTGTGAAAAAGGTATTAGATGAAACGGGTCCGAAAAAAGTGGATATTGTGCGTCA
SEQ: 022-3C12 (151) TGGCCCGGTATTATCTAGATTCTGTCAAAGATGTCTAGACAAAACGGGTCCGAAAAAAGTGGATATTGTGCGTCA
SEQ: 023-3N19 (G2) (151) TGGCCCGGTATTATCACGATTGTGAAAAAGGTATTAGATGAAACCGGTCCGAAAAAAGTGGACATTGTGCGTCA
SEQ: 024-G2.2 (151) TGGCCCGGTATTATCACGATTGTGCAAAAGGTTTAGACGAAACGGGTCCGAAAAAAGTGGATATTGTGCGTCA
SEQ: 025-2C3 (151) TGGCCCGGTATTATCACGATTGTGCAAAAGGTTTAGACGAAACGGGTCCGAAAAAAGTGGATATTGTGCGTCA
SEQ: 026-2F11 (151) TGGCCCGGTATTATCACGATTGTGCAAAAGGTTTAGACGAAACGGGTCCGAAAAAAGTGGATATTGTGCGTCA
SEQ: 027-KV11 (6C7) (151) TGGCCCGGTATTATCACGATTGTGCAAAAGGTTTAGACGAAACGGGTCCGAAAAAAGTGGATATTGTGCGTCA
SEQ: 028-KV6 (3A1) (151) TGGCCCGGTATTATCACGATTGTGCAAAAGGTTTAGACGAAACGGGTCCGAAAAAAGTGGATATTGTGCGTCA
SEQ: 029-KV2 (2D1) (151) TGGCCCGGTATTATCACGATTGTGCAAAAGGTTTAGACGAAACGGGTCCGAAAAAAGTGGATATTGTGCGTCA
SEQ: 030-N2.5 (151) TGGCCCGGTATTATCACGATTGTGCAAAAGGTTTAGACGAAACGGGTCCGAAAAAAGTGGATATTGTGCGTCA
SEQ: 031-KV5 (2H6) (151) TGGCCCGGTATTATCACGATTGTGCAAAAGGTTTAGACGAAACGGGTCCGAAAAAAGTGGATATTGTGCGTCA
SEQ: 032-3E5 (151) TGGCCCGGTATTATCACGATTGTGCAAAAGGTTTAGACGAAACGGGTCCGAAAAAAGTGGATATTGTGCGTCA
SEQ: 033-G2.1 (151) TGGCCCGGTATTATCACGATTGTGCAAAAGGTTTAGACGAAACGGGTCCGAAAAAAGTGGATATTGTGCGTCA
SEQ: 034-3H24 (G2) (151) TGGCCCGGTATTATCACGATTGTGCAAAAGGTTTAGACGAAACGGGTCCGAAAAAAGTGGATATTGTGCGTCA
SEQ: 035-KV10 (4G6) (151) TGGCCCGGTATTATCACGATTGTGCAAAAGGTTTAGACGAAACGGGTCCGAAAAAAGTGGATATTGTGCGTCA
SEQ: 036-KV12 (6D4) (151) TGGCCCGGTATTATCACGATTGTGCAAAAGGTTTAGACGAAACGGGTCCGAAAAAAGTGGATATTGTGCGTCA
SEQ: 037-N2.2 (151) TGGCCCGGTATTATCACGATTGTGCAAAAGGTTTAGACGAAACGGGTCCGAAAAAAGTGGATATTGTGCGTCA
SEQ: 038-N2.3 (151) TGGCCCGGTATTATCACGATTGTGCAAAAGGTTTAGACGAAACGGGTCCGAAAAAAGTGGATATTGTGCGTCA
SEQ: 039-N2.1 (151) TGGCCCGGTATTATCACGATTGTGCAAAAGGTTTAGACGAAACGGGTCCGAAAAAAGTGGATATTGTGCGTCA
SEQ: 040-KV4 (2E12) (151) TGGCCCGGTATTATCACGATTGTGCAAAAGGTTTAGACGAAACGGGTCCGAAAAAAGTGGATATTGTGCGTCA
SEQ: 041-KV9 (4C6) (151) TGGCCCGGTATTATCACGATTGTGCAAAAGGTTTAGACGAAACGGGTCCGAAAAAAGTGGATATTGTGCGTCA
SEQ: 042-7D6 (151) TGGCCCGGTATTATCACGATTGTGCAAAAGGTTTAGACGAAACGGGTCCGAAAAAAGTGGATATTGTGCGTCA
SEQ: 043-3F3 (151) TGGCCCGGTATTATCACGATTGTGCAAAAGGTTTAGACGAAACGGGTCCGAAAAAAGTGGATATTGTGCGTCA
SEQ: 044-2D11 (G2) (151) TGGCCCGGTATTATCACGATTGTGCAAAAGGTTTAGACGAAACGGGTCCGAAAAAAGTGGATATTGTGCGTCA
SEQ: 045-3C23 (G2) (151) TGGCCCGGTATTATCACGATTGTGCAAAAGGTTTAGACGAAACGGGTCCGAAAAAAGTGGATATTGTGCGTCA
SEQ: 046-G2.3 (151) TGGCCCGGTATTATCACGATTGTGCAAAAGGTTTAGACGAAACGGGTCCGAAAAAAGTGGATATTGTGCGTCA
SEQ: 047-2A3 (151) TGGCCCGGTATTATCACGATTGTGCAAAAGGTTTAGACGAAACGGGTCCGAAAAAAGTGGATATTGTGCGTCA
SEQ: 048-2F4 (151) TGGCCCGGTATTATCACGATTGTGCAAAAGGTTTAGACGAAACGGGTCCGAAAAAAGTGGATATTGTGCGTCA
SEQ: 049-2B9 (G2) (151) TGGCCCGGTATTATCACGATTGTGCAAAAGGTTTAGACGAAACGGGTCCGAAAAAAGTGGATATTGTGCGTCA
SEQ: 050-2C5 (151) TGGCCCGGTATTATCACGATTGTGCAAAAGGTTTAGACGAAACGGGTCCGAAAAAAGTGGATATTGTGCGTCA
SEQ: 051-KV1 (2A6) (151) TGGCCCGGTATTATCACGATTGTGCAAAAGGTTTAGACGAAACGGGTCCGAAAAAAGTGGATATTGTGCGTCA
SEQ: 052-2D13 (G2) (151) TGGCCCGGTATTATCACGATTGTGCAAAAGGTTTAGACGAAACGGGTCCGAAAAAAGTGGATATTGTGCGTCA
SEQ: 053-3C8 (151) TGGCCCGGTATTATCACGATTGTGCAAAAGGTTTAGACGAAACGGGTCCGAAAAAAGTGGATATTGTGCGTCA
SEQ: 054-2D5 (151) TGGCCCGGTATTATCACGATTGTGCAAAAGGTTTAGACGAAACGGGTCCGAAAAAAGTGGATATTGTGCGTCA

Figure 4c

SEQ: 021-1f15 (G2) (226) CAGCATGGGCGGCGTAAACACGCTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC
SEQ: 022-3C12 (226) CAGCATGGGCGGCGGAACACACACTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC
SEQ: 023-3N19 (G2) (226) CAGCATGGGTGGCGGAACACACACTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC
SEQ: 024-G2.2 (226) CAGCATGGGCGGCGGAACACACACTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC
SEQ: 025-2C3 (226) CAGCATGGGCGGCGGAACACACACTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC
SEQ: 026-2F11 (226) CAGCATGGGTGGCGGAACACACACTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC
SEQ: 027-KV11 (6C7) (226) CAGTATGGGTGGCGGAACACACACTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC
SEQ: 028-KV6 (3A1) (226) CAGTATGGGTGGCGGAACACACACTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC
SEQ: 029-KV2 (2D1) (226) CAGCATGGGTGGCGGAACACACACTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC
SEQ: 030-N2.5 (226) CAGCATGGGTGGCGGAACACACACTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC
SEQ: 031-KV5 (2H6) (226) CAGCATGGGTGGCGGAACACACACTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC
SEQ: 032-3E5 (226) CAGCATGGGTGGCGGAACACACACTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC
SEQ: 033-G2.1 (226) CAGCATGGGTGGCGGAACACACACTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC
SEQ: 034-3H24 (G2) (226) CAGCATGGGTGGCGGAACACACACTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC
SEQ: 035-KV10 (4G6) (226) CAGCATGGGTGGCGGAACACACACTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC
SEQ: 036-KV12 (6D4) (226) CAGCATGGGTGGCGGAACACACACTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC
SEQ: 037-N2.2 (226) CAGCATGGGTGGCGGAACACACACTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC
SEQ: 038-N2.3 (226) CAGCATGGGTGGCGGAACACACACTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC
SEQ: 039-N2.1 (226) CAGCATGGGTGGCGGAACACACACTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC
SEQ: 040-KV4 (2E12) (226) CAGCATGGGTGGCGGAACACACACTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC
SEQ: 041-KV9 (4C6) (226) CAGCATGGGTGGCGGAACACACACTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC
SEQ: 042-7D6 (226) CAGCATGGGTGGCGGAACACACACTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC
SEQ: 043-3F3 (226) CAGCATGGGTGGCGGAACACACACTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC
SEQ: 044-2D11 (G2) (226) CAGCATGGGTGGCGGAACACACACTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC
SEQ: 045-3C23 (G2) (226) CAGCATGGGTGGCGGAACACACACTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC
SEQ: 046-G2.3 (226) CAGCATGGGTGGCGGAACACACACTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC
SEQ: 047-2A3 (226) CAGCATGGGTGGCGGAACACACACTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC
SEQ: 048-2F4 (226) CAGCATGGGTGGCGGAACACACACTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC
SEQ: 049-2B9 (G2) (226) CAGCATGGGTGGCGGAACACACACTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC
SEQ: 050-2C5 (226) CAGCATGGGTGGCGGAACACACACTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC
SEQ: 051-KV1 (2A6) (226) CAGCATGGGTGGCGGAACACACACTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC
SEQ: 052-2D13 (G2) (226) CAGCATGGGTGGCGGAACACACACTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC
SEQ: 053-3C8 (226) CAGCATGGGTGGCGGAACACACACTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC
SEQ: 054-2D5 (226) CAGCATGGGTGGCGGAACACACACTTTACTACATAAAAAATCTGGACGGCGGGAATAAAGTTGAAAAACGTCGTAAC

Figure 4d

301
 SEQ: 021-1f15 (G2) (301) GCTTGGCGGCACGAACCGTTTCGACGACAAAGCGGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
 SEQ: 022-3C12 (301) GCTTGGCGGCAGAAACCGTTTCGACGACAAAGCGGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
 SEQ: 023-3N19 (G2) (301) GCTTGGCGGCAGAAACCGTTTCGACGACAAAGCGGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
 SEQ: 024-G2.2 (301) GCTTGGCGGCAGAAACCGTTTCGACGACAAAGCGGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
 SEQ: 025-2C3 (301) CATTTGTTGAGACAAACGGACTTCGTTTCAAGCAGAGCATACAGGACAGATCCAAATCAAAAAGATTTTATACAC
 SEQ: 026-2F11 (301) GCTTGGCGGCAGAAACCGTTTCGACGACAAAGCGGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
 SEQ: 027-KV11 (6C7) (301) GCTTGGCGGCAGAAACCGTTTCGACGACAAAGCGGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
 SEQ: 028-KV6 (3A1) (301) GCTTGGCGGCAGAAACCGTTTCGACGACAAAGCGGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
 SEQ: 029-KV2 (2D1) (301) GCTTGGCGGCAGAAACCGTTTCGACGACAAAGCGGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
 SEQ: 030-N2.5 (301) GCTTGGCGGCAGAAACCGTTTCGACGACAAAGCGGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
 SEQ: 031-KV5 (2H6) (301) GCTTGGCGGCAGAAACCGTTTCGACGACAAAGCGGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
 SEQ: 032-3E5 (301) GCTTGGCGGCAGAAACCGTTTCGACGACAAAGCGGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
 SEQ: 033-G2.1 (301) GCTTGGCGGCAGAAACCGTTTCGACGACAAAGCGGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
 SEQ: 034-3H24 (G2) (301) ACTTGGCGGCAGAAACCGTTTCGACGACAAAGCGGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
 SEQ: 035-KV10 (4G6) (301) GCTTGGCGGCAGAAACCGTTTCGACGACAAAGCGGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
 SEQ: 036-KV12 (6D4) (301) GCTTGGCGGCAGAAACCGTTTCGACGACAAAGCGGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
 SEQ: 037-N2.2 (301) GCTTGGCGGCAGAAACCGTTTCGACGACAAAGCGGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
 SEQ: 038-N2.3 (301) GCTTGGCGGCAGAAACCGTTTCGACGACAAAGCGGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
 SEQ: 039-N2.1 (301) GCTTGGCGGCAGAAACCGTTTCGACGACAAAGCGGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
 SEQ: 040-KV4 (2E12) (301) GCTTGGCGGCAGAAACCGTTTCGACGACAAAGCGGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
 SEQ: 041-KV9 (4C6) (301) ACTTGGCGGCAGAAACCGTTTCGACGACAAAGCGGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
 SEQ: 042-7D6 (301) ACTTGGCGGCAGAAACCGTTTCGACGACAAAGCGGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
 SEQ: 043-3F3 (301) GCTTGGCGGCAGAAACCGTTTCGACGACAAAGCGGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
 SEQ: 044-2D11 (G2) (301) ACTTGGCGGCAGAAACCGTTTCGACGACAAAGCGGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
 SEQ: 045-3C23 (G2) (301) ACTTGGCGGCAGAAACCGTTTCGACGACAAAGCGGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
 SEQ: 046-G2.3 (301) GCTTGGCGGCAGAAACCGTTTCGACGACAAAGCGGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
 SEQ: 047-2A3 (301) GCTTGGCGGCAGAAACCGTTTCGACGACAAAGCGGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
 SEQ: 048-2F4 (301) ACTTGGCGGCAGAAACCGTTTCGACGACAAAGCGGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
 SEQ: 049-2B9 (G2) (301) ACTTGGCGGCAGAAACCGTTTCGACGACAAAGCGGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
 SEQ: 050-2C5 (301) ACTTGGCGGCAGAAACCGTTTCGACGACAAAGCGGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
 SEQ: 051-KV1 (2A6) (301) GCTTGGCGGCAGAAACCGTTTCGACGACAAAGCGGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
 SEQ: 052-2D13 (G2) (301) GCTTGGCGGCAGAAACCGTTTCGACGACAAAGCGGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
 SEQ: 053-3C8 (301) ACTTGGCGGCAGAAACCGTTTCGACGACAAAGCGGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC
 SEQ: 054-2D5 (301) ACTTGGCGGCAGAAACCGTTTCGACGACAAAGCGGCTTCCGGGAACAGATCCAAATCAAAAAGATTTTATACAC

Figure 4e

SEQ: 021-1f15 (G2) (376) ATCCATTACAGCAGTCCGATATGATTGTCAATGAATTACTTTATCAAAATTTAGACGGTGC'TAAAAAATGTTCAAAAT
 SEQ: 022-3C12 (376) ATCCATTACAGCAGTCCGATATGATTGTCAATGAATTACTTTATCAAAATTTAGACGGGCTAAAAAATGTTCAAAAT
 SEQ: 023-3N19 (G2) (376) ATCCATTACGGCAGTCCGATATGATTGTCAATGAATTACTTTATCAAAATTTAGACGGTGC'TAAAAAATGTTCAAAAT
 SEQ: 024-G2.2 (376) ATCCATTACGGCAGTCCGATATGATTGTCAATGAATTACTTTATCAAAATTTAGACGGTGC'TAAAAAATGTTCAAAAT
 SEQ: 025-2C3 (376) ATCCGTCATAGCTCAGCATCTTATTGTGCTCAACAGCTCTCTCGTTTAAATTTGGCGCAAGAAACGTTCCAAAT
 SEQ: 026-2F11 (376) ATCCATTACAGCAGTCCGATATGATTGTCAATGAATTACTTTATCAAAATTTAGACGGTGC'TAAAAAATGTTCAAAAT
 SEQ: 027-KV11 (6C7) (376) ATCCGTTTACAGTAGTGTGATGATTGTATGAATTACTTTATCAAAATTTAGACGGGCTAAAAAATGTTCAAAAT
 SEQ: 028-KV6 (3A1) (376) ATCCGTTTACAGTAGTGTGATGATTGTATGAATTACTTTATCAAAATTTAGACGGGCTAAAAAATGTTCAAAAT
 SEQ: 029-KV2 (2D1) (376) ATCCGTTTACAGTAGTGTGATGATTGTATGAATTACTTTATCAAAATTTAGACGGGCTAAAAAATGTTCAAAAT
 SEQ: 030-N2.5 (376) ATCCGTTTACAGTAGTGTGATGATTGTATGAATTACTTTATCAAAATTTAGACGGGCTAAAAAATGTTCAAAAT
 SEQ: 031-KV5 (2H6) (376) ATCCGTTTACAGCAGTCCGATATGATTGTCAATGAATTACTTTATCAAAATTTAGACGGTGC'TAAAAAATGTTCAAAAT
 SEQ: 032-3E5 (376) ATCCATTACAGCAGTCCGATATGATTGTCAATGAATTACTTTATCAAAATTTAGACGGGCTAAAAAATGTTCAAAAT
 SEQ: 033-G2.1 (376) ATCCATTACAGCAGTCCGATATGATTGTCAATGAATTACTTTATCAAAATTTAGACGGTGC'TAAAAAATGTTCAAAAT
 SEQ: 034-3H24 (G2) (376) ATCCATTACAGCAGTCCGATATGATTGTCAATGAATTACTTTATCAAAATTTAGACGGTGC'TAAAAAATGTTCAAAAT
 SEQ: 035-KV10 (4G6) (376) ATCCATTACAGCAGTCCGATATGATTGTCAATGAATTACTTTATCAAAATTTAGACGGTGC'TAAAAAATGTTCAAAAT
 SEQ: 036-KV12 (6D4) (376) ATCCGTTTACAGCAGTCCGATATGATTGTCAATGAATTACTTTATCAAAATTTAGACGGTGC'TAAAAAATGTTCAAAAT
 SEQ: 037-N2.2 (376) ATCCGTTTACAGCAGTCCGATATGATTGTCAATGAATTACTTTATCAAAATTTAGACGGTGC'TAAAAAATGTTCAAAAT
 SEQ: 038-N2.3 (376) ATCCGTTTACAGCAGTCCGATATGATTGTCAATGAATTACTTTATCAAAATTTAGACGGTGC'TAAAAAATGTTCAAAAT
 SEQ: 039-N2.1 (376) ATCCGTTTACAGCAGTCCGATATGATTGTCAATGAATTACTTTATCAAAATTTAGACGGTGC'TAAAAAATGTTCAAAAT
 SEQ: 040-KV4 (2E12) (376) ATCCATTACAGCAGTCCGATATGATTGTCAATGAATTACTTTATCAAAATTTAGACGGTGC'TAAAAAATGTTCAAAAT
 SEQ: 041-KV9 (4C6) (376) ATCCATTACAGCAGTCCGATATGATTGTCAATGAATTACTTTATCAAAATTTAGACGGGCTAAAAAATGTTCAAAAT
 SEQ: 042-7D6 (376) ATCCATTACAGCAGTCCGATATGATTGTCAATGAATTACTTTATCAAAATTTAGACGGTGC'TAAAAAATGTTCAAAAT
 SEQ: 043-3F3 (376) ATCCATTACAGCAGTCCGATATGATTGTCAATGAATTACTTTATCAAAATTTAGACGGTGC'TAAAAAATGTTCAAAAT
 SEQ: 044-2D11 (G2) (376) ATCCATTACAGCAGTCCGATATGATTGTCAATGAATTACTTTATCAAAATTTAGACGGTGC'TAAAAAATGTTCAAAAT
 SEQ: 045-3C23 (G2) (376) ATCCATTACAGCAGTCCGATATGATTGTCAATGAATTACTTTATCAAAATTTAGACGGTGC'TAAAAAATGTTCAAAAT
 SEQ: 046-G2.3 (376) ATCCATTACAGCAGTCCGATATGATTGTCAATGAATTACTTTATCAAAATTTAGACGGTGC'TAAAAAATGTTCAAAAT
 SEQ: 047-2A3 (376) ATCCGTTTACAGTAGTGTGATGATTGTATGAATTACTTTATCAAAATTTAGACGGTGC'TAAAAAATGTTCAAAAT
 SEQ: 048-2F4 (376) ATCCGTTTACAGTAGTGTGATGATTGTATGAATTACTTTATCAAAATTTAGACGGTGC'TAAAAAATGTTCAAAAT
 SEQ: 049-2B9 (G2) (376) ATCCATTACAGCAGTCCGATATGATTGTCAATGAATTACTTTATCAAAATTTAGACGGGCTAAAAAATGTTCAAAAT
 SEQ: 050-2C5 (376) ATCCATTACAGCAGTCCGATATGATTGTCAATGAATTACTTTATCAAAATTTAGACGGTGC'TAAAAAATGTTCAAAAT
 SEQ: 051-KV1 (2A6) (376) ATCCATTACAGCAGTCCGATATGATTGTCAATGAATTACTTTATCAAAATTTAGACGGTGC'TAAAAAATGTTCAAAAT
 SEQ: 052-2D13 (G2) (376) ATCCATTACAGCAGTCCGATATGATTGTCAATGAATTACTTTATCAAAATTTAGACGGTGC'TAAAAAATGTTCAAAAT
 SEQ: 053-3C8 (376) ATCCATTACAGCAGTCCGATATGATTGTCAATGAATTACTTTATCAAAATTTAGACGGTGC'TAAAAAATGTTCAAAAT
 SEQ: 054-2D5 (376) ATCCATTACAGCAGTCCGATATGATTGTCAATGAATTACTTTATCAAAATTTAGACGGTGC'TAAAAAATGTTCAAAAT

Figure 4 f

SEQ: 021-1f15 (G2) (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAAGGACTGAACGGCGG
 SEQ: 022-3C12 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAAGGACTGAACGGCGG
 SEQ: 023-3N19 (G2) (451) CCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAAGGACTGAACGGCGG
 SEQ: 024-G2.2 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAAGGACTGAACGGCGG
 SEQ: 025-2C3 (451) CCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAAGGACTGAACGGCGG
 SEQ: 026-2F11 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAAGGACTGAACGGCGG
 SEQ: 027-KV11 (6C7) (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAAGGACTGAACGGCGG
 SEQ: 028-KV6 (3A1) (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAAGGACTGAACGGCGG
 SEQ: 029-KV2 (2D1) (451) TCATGGTGTGGGCACATTTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAAGGACTGAACGGCGG
 SEQ: 030-N2.5 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAAGGACTGAACGGCGG
 SEQ: 031-KV5 (2H6) (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAAGGACTGAACGGCGG
 SEQ: 032-3E5 (451) CCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAAGGACTGAACGGCGG
 SEQ: 033-G2.1 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAAGGACTGAACGGCGG
 SEQ: 034-3H24 (G2) (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAAGGACTGAACGGCGG
 SEQ: 035-KV10 (4G6) (451) CCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAAGGACTGAACGGCGG
 SEQ: 036-KV12 (6D4) (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAAGGACTGAACGGCGG
 SEQ: 037-N2.2 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAAGGACTGAACGGCGG
 SEQ: 038-N2.3 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAAGGACTGAACGGCGG
 SEQ: 039-N2.1 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAAGGACTGAACGGCGG
 SEQ: 040-KV4 (2E12) (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAAGGACTGAACGGCGG
 SEQ: 041-KV9 (4C6) (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAAGGACTGAACGGCGG
 SEQ: 042-7D6 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAAGGACTGAACGGCGG
 SEQ: 043-3F3 (451) CCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAAGGACTGAACGGCGG
 SEQ: 044-2D11 (G2) (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAAGGACTGAACGGCGG
 SEQ: 045-3C23 (G2) (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAAGGACTGAACGGCGG
 SEQ: 046-G2.3 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAAGGACTGAACGGCGG
 SEQ: 047-2A3 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAAGGACTGAACGGCGG
 SEQ: 048-2F4 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAAGGACTGAACGGCGG
 SEQ: 049-2B9 (G2) (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAAGGACTGAACGGCGG
 SEQ: 050-2C5 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAAGGACTGAACGGCGG
 SEQ: 051-KV1 (2A6) (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAAGGACTGAACGGCGG
 SEQ: 052-2D13 (G2) (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAAGGACTGAACGGCGG
 SEQ: 053-3C8 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAAGGACTGAACGGCGG
 SEQ: 054-2D5 (451) TCATGGCGTTGGGCACATTTGGTTTATTGATGAACAGCCAAAGTCAACAGCCTGATTTAAAGAAAGGACTGAACGGCGG

Figure 4g

	526	544
SEQ: 021-1f15 (G2)	(526)	GGGACTCAATACGAATTGA
SEQ: 022-3C12	(526)	GGGACTCAATACGAATTGA
SEQ: 023-3N19 (G2)	(526)	GGGACTGAATACAAAATTGA
SEQ: 024-G2.2	(526)	GGGACTCAATACGAATTGA
SEQ: 025-2C3	(526)	GGGCCACAATACGAATTGA
SEQ: 026-2F11	(526)	AGGCTAAATACGAATTGA
SEQ: 027-KV11 (6C7)	(526)	GGGCTTAAATACAAAATTGA
SEQ: 028-KV6 (3A1)	(526)	GGGCTTAAATACAAAATTGA
SEQ: 029-KV2 (2D1)	(526)	GGGCCAAAATACAAAATTGA
SEQ: 030-N2.5	(526)	GGGCCACAATACAAAATTGA
SEQ: 031-KV5 (2H6)	(526)	GGGCTGAATACAAAATTGA
SEQ: 032-3E5	(526)	GGGCTCAATACGAATTGA
SEQ: 033-G2.1	(526)	GGGACTCAATACGAATTGA
SEQ: 034-3H24 (G2)	(526)	GGGACTCAATACGAATTGA
SEQ: 035-KV10 (4G6)	(526)	GGGCCACAATACAAAATTGA
SEQ: 036-KV12 (6D4)	(526)	AGGCCACAATACAAAATTGA
SEQ: 037-N2.2	(526)	AGGCCACAATACAAAATTGA
SEQ: 038-N2.3	(526)	AGGCCACAATACAAAATTGA
SEQ: 039-N2.1	(526)	AGGCCACAATACAAAATTGA
SEQ: 040-KV4 (2E12)	(526)	GGGCCACAATACAAAATTGA
SEQ: 041-KV9 (4C6)	(526)	GGGCCACAATACGAATTGA
SEQ: 042-7D6	(526)	GGGATTAAATACGAATTGA
SEQ: 043-3F3	(526)	GGGCCAGAATACGAATTGA
SEQ: 044-2D11 (G2)	(526)	AGGCCAGAATACGAATTGA
SEQ: 045-3C23 (G2)	(526)	GGGCCACAATACGAATTGA
SEQ: 046-G2.3	(526)	GGGCCAGAATACGAATTGA
SEQ: 047-2A3	(526)	AGGCTTAAATACAAAATTGA
SEQ: 048-2F4	(526)	AGGCCAGAATACGAATTGA
SEQ: 049-2B9 (G2)	(526)	AGGCCAAAATACGAATTGA
SEQ: 050-2C5	(526)	AGGCCAAAATACGAATTGA
SEQ: 051-KV1 (2A6)	(526)	GGGCCAGAATACGAATTGA
SEQ: 052-2D13 (G2)	(526)	AGGCCAAAATACGAATTGA
SEQ: 053-3C8	(526)	GGGCCAAAATACAAAATTGA
SEQ: 054-2D5	(526)	AGGACAAAATACAAAATTGA

Figure 4 h

	-35	-1	1	40
SEQ: 055-405 (pumilus)	(1)	--MKFVKRRIIALVTILVLSVTSLFAMQP-SAKAA	EHNPPVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDF	
SEQ: 056-406 (subtilis)	(1)	--MKFVKRRIIALVTILMLSVTSLFALQP-SAKAA	EHNPPVMVHGIGGASFNFAGIKSYLVSQGWSRDKLYAVDF	
SEQ: 057-402 (megat.)	(1)	--MKFVKRRIIALVTILVLSVTSLFAMQP-SAKAA	DTIQLLWFTGIGGASYNFAGIKSYLVSQGWSRGKLYAVDF	
SEQ: 058-400 (lentus)	(1)	--MKFVKRRIIALVTILVLSVTSLFAMQP-SAKAA	EHNPPVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDF	
SEQ: 059-396 (clarcul.)	(1)	--MKFIKRRIIALVTILVLSVTSLFAMQP-SAKAA	EHNPPVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDF	
SEQ: 060-392 (azotof.)	(1)	--MKFVKRRIIALVTILVLSVTSLFAMQP-SAKAA	EHNPPVMVHGIGGASYNFAGIKSYLVSQGWSRGELYAVDF	
SEQ: 061-398 (firmus)	(1)	--MKFVKRRIIALVTILVLSVTSLFAMQP-SAKAA	EHNPPVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDF	
SEQ: 062-393 (badius)	(1)	--MKFVKRRIIALVTILVLSVTSLFAMQP-SAKAA	EHNPPVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDF	
SEQ: 063-Dc5h	(1)	--MKFVKRRIIALVTILMLSVTSLFALQP-SAKAA	EHNPPVMVHGIGGASFNFAGIKSYLVSQGWSRDKLYAVDF	
SEQ: 064-Dc5f	(1)	--MKFVKRRIIALVTILMLSVTSLFALQP-SAKAA	EHNPPVMVHGIGGASFNFAGIKSYLVSQGWSRDKLYAVDF	
SEQ: 065-Dc5c1	(1)	MKVI FVKRSLQILVALALVLSIAFIQPKAEKAA	EHNPPVMVHGMGGASYNFASIKRYLVSQGWDQNQLFAIDF	
SEQ: 066-Dc5a2	(1)	MKVI FVKRSLQILVVALVMGSMAFIQPKEIRAA	EHNPPVMVHGMGGASYNFASIKSYLVSQGWDNRNQLFAIDF	
SEQ: 067-Dc512	(1)	MKVI FVKRSLQILIALALVIGSMAFIQPKEAKAA	EHNPPVMVHGIGGASYNFFSIKSYLATQGWDNRNQLYALDF	
SEQ: 068-Sga	(1)	--MKFVKRRIIALVTILMLSVTSLFALQP-SAKAA	EHNPPVMVHGIGGASFNFAGIKSYLVSQGWSRDKLYAVDF	
SEQ: 069-Sgc	(1)	--MKFVKRRIIALVTILMLSVTSLFALQP-SAKAA	EHNPPVMVHGIGGASFNFAGIKSYLVSQGWSRDKLYAVDF	
SEQ: 070-Sgd	(1)	--MKFVKRRIIALVTILMLSVTSLFALQP-SAKAA	EHNPPVMVHGIGGASFNFAGIKSYLVSQGWSRDKLYAVDF	
SEQ: 071-Sgf	(1)	--MKFVKRRIIALVTILMLSVTSLFALQP-SAKAA	EHNPPVMVHGIGGASFNFAGIKSYLVSQGWSRDKLYAVDF	
SEQ: 072-Sgh	(1)	--MKFVKRRIIALVTILMLSVTSLFALQP-SAKAA	EHNPPVMVHGIGGASFNFAGIKSYLVSQGWSRDKLYAVDF	
SEQ: 073-Mc2b1	(1)	MKVI FVKRSLQILVALALVIGSMAFIQPKEIKAA	EHNPPVMVHGIGGASYNFASIKSYLVNQGWDNRNQLFAIDF	
SEQ: 074-H2a	(1)	--MKFVKRRIIALVTILMLSVTSLFALQP-SAKAA	EHNPPVMVHGIGGASFNFAGIKSYLVSQGWSRDKLYAVDF	

Figure 5a

41

SEQ: 055-405 (pumilus)	(73)	WDKTGTNYNNGPVL	SRFVQKVL	DETGA	KKVD	IVAH	SMGGANT	PYYI	KNLD	GGNKI	ENVV	TL	GGAN	STTS	KALPG
SEQ: 056-406 (subtilis)	(73)	WDKTGTNYNNGPVL	PRFVQKVL	DETGA	KKVD	IVAH	SMGGANT	LYI	KNLD	GGNKV	ANV	VT	TL	GGAN	LT
SEQ: 057-402 (megat.)	(73)	WDKTGTNYNNGPVL	SRFVQKVL	DETGA	KKVD	IVAH	SMGGANT	LYI	KNLD	GGNKI	ENV	VT	TL	GGAN	LT
SEQ: 058-400 (lentus)	(73)	WDKTGTNYNNGPVL	SRFVQKVL	DETGA	KKVD	IVAH	SMGGANT	LYI	KNLD	GGNKI	ENV	VT	TL	GGAN	LT
SEQ: 059-396 (circul.)	(73)	WDKTGTNYNNGPVL	SRFVQKVL	DETGA	KKVD	IVAH	SMGGANT	LYI	KNLD	GGNKI	ENV	VT	TL	GGAN	LT
SEQ: 060-392 (azotof.)	(73)	WDKTGTNYNNGPVL	SRFVQKVL	DETGA	KKVD	IVAH	SMGGANT	LYI	KNLD	GGNKI	ENV	VT	TL	GGAN	LT
SEQ: 061-398 (firmus)	(73)	WDKTGTNYNNGPVL	SRFVQKVL	DETGA	KKVD	IVAH	SMGGANT	LYI	KNLD	GGNKI	ENV	VT	TL	GGAN	LT
SEQ: 062-393 (badius)	(73)	WDKTGTNYNNGPVL	SRFVQKVL	DETGA	KKVD	IVAH	SMGGANT	LYI	KNLD	GGNKI	ENV	VT	TL	GGAN	LT
SEQ: 063-Dc5h	(73)	KDKTGTNYNNGPVL	SRFVQKVL	DETGA	KKVD	IVAH	SMGGANT	LYI	KNLD	GGNKI	ENV	VT	TL	GGAN	LT
SEQ: 064-Dc5f	(73)	XDKTGNNRNGPRL	SRFVKDVL	DKTGA	KKVD	IVAH	SMGGANT	LYI	KNLD	GGNKV	ENV	VT	TL	GGAN	LT
SEQ: 065-Dc5c1	(76)	IDKTGNNLNGPRL	SRFVKDVL	LAKTGA	KKVD	IVAH	SMGGANT	LYI	KNLD	GGDKI	ENV	VT	TL	GGAN	LV
SEQ: 066-Dc5a2	(76)	IDKTGNNRNGPRL	SRFVKDVL	LAKTGA	KKVD	IVAH	SMGGANT	LYI	KNLD	GGDKI	ENV	VT	TL	GGAN	LV
SEQ: 067-Dc512	(76)	IDKTGNNRNGPRL	SRFVKDVL	DKTGA	KKVD	IVAH	SMGGANT	LYI	KNLD	GGDKI	ENV	VT	TL	GGAN	LV
SEQ: 068-Sga	(73)	RDKTGNNLNGPVL	SRFVKDVL	DETGA	KKVD	IVAH	SMGGANT	LYI	KNLD	GGNKI	ENV	VT	TL	GGAN	LV
SEQ: 069-Sgc	(73)	WDKTGNNLNGPVL	SRFVKDVL	DETGA	KKVD	IVAH	SMGGANT	LYI	KNLD	GGNKI	ENV	VT	TL	GGAN	LV
SEQ: 070-Sgd	(73)	SDKTGNNLNGPVL	SRFVKDVL	DETGA	KKVD	IVAH	SMGGANT	LYI	KNLD	GGNKI	ENV	VT	TL	GGAN	LV
SEQ: 071-Sgf	(73)	KDKTGNNRNGPRL	SRFVKDVL	DKTGA	KKVD	IVAH	SMGGANT	LYI	KNLD	GGDKI	ENV	VT	TL	GGAN	LV
SEQ: 072-Sgh	(73)	IDKTGNNRNGPRL	SRFVKDVL	DKTGA	KKVD	IVAH	SMGGANT	LYI	KNLD	GGDKI	ENV	VT	TL	GGAN	LV
SEQ: 073-Mt2b1	(76)	IDKTGNNRNGPRL	SRFVKDVL	DKTGA	KKVD	IVAH	SMGGANT	LYI	KNLD	GGDKI	ENV	VT	TL	GGAN	LV
SEQ: 074-H2a	(73)	RDKTGNNRNGPRL	SKFVKDVL	DKTGA	KKVD	IVAH	SMGGANT	LYI	KNLD	GGDKI	ENV	VT	TL	GGAN	LV

Figure 5b

SEQ: 055-405 (pumilus)	(148)	116	TDPNQKILYTSIYSSADMIVMN- YLSKLDGAKNAQIHGVGHI GLLMNSQVNSLIKEGLNGGGQNTN	181
SEQ: 056-406 (subtilis)	(148)		TDPNQKILYTSIYSSADMIVN- YLSRLDGARNVQIHGVGHI GLLYSSQVNSLIKEGLNGGGGLNTN	
SEQ: 057-402 (megat.)	(148)		TDPNQKILYTSIYSSADMIVMN- YLSKLDGAKNVQIHGVGHI GLLMNSQVNSLIKEGLNGGGHNTN	
SEQ: 058-400 (lentus)	(148)		TDPNQKILYTSIYSSADMIVMN- YLSKLDGAKNVQIHGVGHI GLLMNSQVNSLIKEGLNGGGGLNTN	
SEQ: 059-396 (circul.)	(148)		TDPNQKILYTSIYSSADMIVMN- YLSKLDGAKNVQIHGVGHI GLLMNSQVNSLIKEGLNGGGGLNTN	
SEQ: 060-392 (azotof.)	(148)		TDPNQKILYTSIYSSADMIVMN- YLSKLDGAKNVQIHGVGHI GLLMNSQVNSLIKEGLNGGGGLDTN	
SEQ: 061-398 (firmus)	(148)		TDPNQKILYTSIYSSADMIVMN- YLSKLDGAKNAQIHGVGHI GLLMNSQVNSLIKEGLNGGGHNTN	
SEQ: 062-393 (badius)	(148)		TDPNQKILYTSIYSSADMIVMN- YLSKLDGAKNVQIHGVGHI GLLMNSQVNSLIKEGLNGGGHNTN	
SEQ: 063-Dc5h	(148)		TDPNQKILYTSIYSSADMIVMN- YLSRLDGARNVQIHGVGHI GLLYSSQVNSLIKEGLNGGGGLNTN	
SEQ: 064-Dc5f	(148)		TDPNQKILYTSVYSSADLIVVN- SLSRLIGARNLIGHGVGHI GLTSSQVKGYIKEGLNGGGGLNTN	
SEQ: 065-Dc5c1	(151)		TDPNQKILYTSVYSSADLIVVN- SLSRLIGARNLIGHGVGHI GLTSSQVKGYIKEGLNGGGQNTN	
SEQ: 066-Dc5a2	(151)		TDPNQKILYTSVYSSADLIVVN- SLSRLIGARNLIGHGVGHI GLTSSQVKGYIKEGLNGGGQNTN	
SEQ: 067-Dc512	(151)		TDPNQKILYTSVYSSADLIVVN- SLSQFNWRKKHPDPGVGHI GLTSSQVKGYIKEGLNGGGGLNTN	
SEQ: 068-Sga	(148)		TDPNQKILYTSVYSSADMIVMN- YLTCLDGAKNVQIHGVGHI GLLYSSQVNSLIKEGLNGGGGLNTN	
SEQ: 069-Sgc	(148)		TDPNQKILYTSVYSSADMIVMN- YLSKLDGAKNVQIHGVGHI GLLYSSQVNSLIKEGLNGGGGLNTN	
SEQ: 070-Sgd	(148)		TDPNQKILYTSVYSSADLIVVN- SLSRLIGARNVQIHGVGHI GLTSSQVKGYIKEGLNGGGGLNTN	
SEQ: 071-Sgf	(148)		TDPNQKILYTSVYSSADLIVVN- SLSRLIGARNVQIHGVGHI GLTSSQVKGYIKEGLNGGGGLNTN	
SEQ: 072-Sgh	(148)		TDPNQKILYTSVYSSADLIVVN- SLSRLIGARNVQIHGVGHI GLTSSQVKGYIKEGLNGGGQNTN	
SEQ: 073-Mt2b1	(151)		TDPNQKILYTSVYSSADLIVVN- SLSRLTGARNLIGHGVGHI GLTSSQVKGYIKEGLNGGGGLNTN	
SEQ: 074-H2a	(148)		TDPNQKILYTSVKLSRSHCRQQLSFNWLQETVQIHGVGHI GLTSSQVKGYIKEGLNGGGGLNTN	

Figure 5c

SEQ: 075-1f15 (G2)	1	EHN	PV	VM	VH	GI	GG	AS	FN	FA	GI	KS	YL	VS	QW	SR	GL	YA	VD	FW	DK	TG	TN	YNN	GP	VL	SR	FV	QV	KL	DE	TG	AK	KV	D	I	VA	H
SEQ: 076-3C12	(1)	EHN	PV	VM	VH	GI	GG	AS	FN	FA	GI	KS	YL	VS	QW	SR	GL	YA	VD	FW	DK	TG	TN	YNN	GP	VL	SR	FV	QV	KL	DE	TG	AK	KV	D	I	VA	H
SEQ: 077-3N19 (G2)	(1)	EHN	PV	VM	VH	GI	GG	AS	FN	FA	GI	KS	YL	VS	QW	SR	GL	YA	VD	FW	DR	TG	TN	YNN	GP	VL	SR	FV	QV	KL	DE	TG	AK	KV	D	I	VA	H
SEQ: 078-G2.2	(1)	EHN	PV	VM	VH	GI	GG	AS	FN	FA	GI	KS	YL	VS	QW	SR	GL	YA	VD	FW	DK	TG	TN	YNN	GP	VL	SR	FV	QV	KL	DE	TG	AK	KV	D	I	VA	H
SEQ: 079-2C3	(1)	EHN	PV	VM	VH	GI	GG	AS	FN	FA	GI	KS	YL	VS	QW	SR	GL	YA	VD	FW	DK	TG	TN	YNN	GP	VL	SR	FV	QV	KL	DE	TG	AK	KV	D	I	VA	H
SEQ: 080-2F11	(1)	EHN	PV	VM	VH	GI	GG	AS	FN	FA	GI	KS	YL	VS	QW	SR	GL	YA	VD	FW	DK	TG	TN	YNN	GP	VL	SR	FV	QV	KL	DE	TG	AK	KV	D	I	VA	H
SEQ: 081-KV11 (6C7)	(1)	EHN	PV	VM	VH	GI	GG	AS	FN	FA	GI	KS	YL	VS	QW	SR	GL	YA	VD	FW	DK	TG	TN	YNN	GP	VL	SR	FV	QV	KL	DE	TG	AK	KV	D	I	VA	H
SEQ: 082-KV6 (3A1)	(1)	EHN	PV	VM	VH	GI	GG	AS	FN	FA	GI	KS	YL	VS	QW	SR	GL	YA	VD	FW	DK	TG	TN	YNN	GP	VL	SR	FV	QV	KL	DE	TG	AK	KV	D	I	VA	H
SEQ: 083-KV2 (2D1)	(1)	EHN	PV	VM	VH	GI	GG	AS	FN	FA	GI	KS	YL	VS	QW	SR	GL	YA	VD	FW	DK	TG	TN	YNN	GP	VL	SR	FV	QV	KL	DE	TG	AK	KV	D	I	VA	H
SEQ: 084-N2.5	(1)	EHN	PV	VM	VH	GI	GG	AS	FN	FA	GI	KS	YL	VS	QW	SR	GL	YA	VD	FW	DK	TG	TN	YNN	GP	VL	SR	FV	QV	KL	DE	TG	AK	KV	D	I	VA	H
SEQ: 085-KV5 (2H6)	(1)	EHN	PV	VM	VH	GI	GG	AS	FN	FA	GI	KS	YL	VS	QW	SR	GL	YA	VD	FW	DK	TG	TN	YNN	GP	VL	SR	FV	QV	KL	DE	TG	AK	KV	D	I	VA	H
SEQ: 086-3E5	(1)	EHN	PV	VM	VH	GI	GG	AS	FN	FA	GI	KS	YL	VS	QW	SR	GL	YA	VD	FW	DK	TG	TN	YNN	GP	VL	SR	FV	QV	KL	DE	TG	AK	KV	D	I	VA	H
SEQ: 087-G2.1	(1)	EHN	PV	VM	VH	GI	GG	AS	FN	FA	GI	KS	YL	VS	QW	SR	GL	YA	VD	FW	DK	TG	TN	YNN	GP	VL	SR	FV	QV	KL	DE	TG	AK	KV	D	I	VA	H
SEQ: 088-3H24 (G2)	(1)	EHN	PV	VM	VH	GI	GG	AS	FN	FA	GI	KS	YL	VS	QW	SR	GL	YA	VD	FW	DK	TG	TN	YNN	GP	VL	SR	FV	QV	KL	DE	TG	AK	KV	D	I	VA	H
SEQ: 089-KV10 (4G6)	(1)	EHN	PV	VM	VH	GI	GG	AS	FN	FA	GI	KS	YL	VS	QW	SR	GL	YA	VD	FW	DK	TG	TN	YNN	GP	VL	SR	FV	QV	KL	DE	TG	AK	KV	D	I	VA	H
SEQ: 090-KV12 (6D4)	(1)	EHN	PV	VM	VH	GI	GG	AS	FN	FA	GI	KS	YL	VS	QW	SR	GL	YA	VD	FW	DK	TG	TN	YNN	GP	VL	SR	FV	QV	KL	DE	TG	AK	KV	D	I	VA	H
SEQ: 091-N2.2	(1)	EHN	PV	VM	VH	GI	GG	AS	FN	FA	GI	KS	YL	VS	QW	SR	GL	YA	VD	FW	DK	TG	TN	YNN	GP	VL	SR	FV	QV	KL	DE	TG	AK	KV	D	I	VA	H
SEQ: 092-N2.3	(1)	EHN	PV	VM	VH	GI	GG	AS	FN	FA	GI	KS	YL	VS	QW	SR	GL	YA	VD	FW	DK	TG	TN	YNN	GP	VL	SR	FV	QV	KL	DE	TG	AK	KV	D	I	VA	H
SEQ: 093-N2.1	(1)	EHN	PV	VM	VH	GI	GG	AS	FN	FA	GI	KS	YL	VS	QW	SR	GL	YA	VD	FW	DK	TG	TN	YNN	GP	VL	SR	FV	QV	KL	DE	TG	AK	KV	D	I	VA	H
SEQ: 094-KV4 (2E12)	(1)	EHN	PV	VM	VH	GI	GG	AS	FN	FA	GI	KS	YL	VS	QW	SR	GL	YA	VD	FW	DK	TG	TN	YNN	GP	VL	SR	FV	QV	KL	DE	TG	AK	KV	D	I	VA	H
SEQ: 095-KV9 (4C6)	(1)	EHN	PV	VM	VH	GI	GG	AS	FN	FA	GI	KS	YL	VS	QW	SR	GL	YA	VD	FW	DK	TG	TN	YNN	GP	VL	SR	FV	QV	KL	DE	TG	AK	KV	D	I	VA	H
SEQ: 096-7D6	(1)	EHN	PV	VM	VH	GI	GG	AS	FN	FA	GI	KS	YL	VS	QW	SR	GL	YA	VD	FW	DK	TG	TN	YNN	GP	VL	SR	FV	QV	KL	DE	TG	AK	KV	D	I	VA	H
SEQ: 097-3F3	(1)	EHN	PV	VM	VH	GI	GG	AS	FN	FA	GI	KS	YL	VS	QW	SR	GL	YA	VD	FW	DK	TG	TN	YNN	GP	VL	SR	FV	QV	KL	DE	TG	AK	KV	D	I	VA	H
SEQ: 098-2D11 (G2)	(1)	EHN	PV	VM	VH	GI	GG	AS	FN	FA	GI	KS	YL	VS	QW	SR	GL	YA	VD	FW	DK	TG	TN	YNN	GP	VL	SR	FV	QV	KL	DE	TG	AK	KV	D	I	VA	H
SEQ: 099-3C23 (G2)	(1)	EHN	PV	VM	VH	GI	GG	AS	FN	FA	GI	KS	YL	VS	QW	SR	GL	YA	VD	FW	DK	TG	TN	YNN	GP	VL	SR	FV	QV	KL	DE	TG	AK	KV	D	I	VA	H
SEQ: 100-G2.3	(1)	EHN	PV	VM	VH	GI	GG	AS	FN	FA	GI	KS	YL	VS	QW	SR	GL	YA	VD	FW	DK	TG	TN	YNN	GP	VL	SR	FV	QV	KL	DE	TG	AK	KV	D	I	VA	H
SEQ: 101-2A3	(1)	EHN	PV	VM	VH	GI	GG	AS	FN	FA	GI	KS	YL	VS	QW	SR	GL	YA	VD	FW	DK	TG	TN	YNN	GP	VL	SR	FV	QV	KL	DE	TG	AK	KV	D	I	VA	H
SEQ: 102-2F4	(1)	EHN	PV	VM	VH	GI	GG	AS	FN	FA	GI	KS	YL	VS	QW	SR	GL	YA	VD	FW	DK	TG	TN	YNN	GP	VL	SR	FV	QV	KL	DE	TG	AK	KV	D	I	VA	H
SEQ: 103-2B9 (G2)	(1)	EHN	PV	VM	VH	GI	GG	AS	FN	FA	GI	KS	YL	VS	QW	SR	GL	YA	VD	FW	DK	TG	TN	YNN	GP	VL	SR	FV	QV	KL	DE	TG	AK	KV	D	I	VA	H
SEQ: 104-2C5	(1)	EHN	PV	VM	VH	GI	GG	AS	FN	FA	GI	KS	YL	VS	QW	SR	GL	YA	VD	FW	DK	TG	TN	YNN	GP	VL	SR	FV	QV	KL	DE	TG	AK	KV	D	I	VA	H
SEQ: 105-KV1 (2A6)	(1)	EHN	PV	VM	VH	GI	GG	AS	FN	FA	GI	KS	YL	VS	QW	SR	GL	YA	VD	FW	DK	TG	TN	YNN	GP	VL	SR	FV	QV	KL	DE	TG	AK	KV	D	I	VA	H
SEQ: 106-2D13 (G2)	(1)	EHN	PV	VM	VH	GI	GG	AS	FN	FA	GI	KS	YL	VS	QW	SR	GL	YA	VD	FW	DK	TG	TN	YNN	GP	VL	SR	FV	QV	KL	DE	TG	AK	KV	D	I	VA	H
SEQ: 107-3C8	(1)	EHN	PV	VM	VH	GI	GG	AS	FN	FA	GI	KS	YL	VS	QW	SR	GL	YA	VD	FW	DK	TG	TN	YNN	GP	VL	SR	FV	QV	KL	DE	TG	AK	KV	D	I	VA	H
SEQ: 108-2D5	(1)	EHN	PV	VM	VH	GI	GG	AS	FN	FA	GI	KS	YL	VS	QW	SR	GL	YA	VD	FW	DK	TG	TN	YNN	GP	VL	SR	FV	QV	KL	DE	TG	AK	KV	D	I	VA	H

Figure 6a

SEQ: 075-1f15 (G2) (76) SMGGANTL YYIKNLDGKNKVENVVTLGGTNRSTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 076-3C12 (76) SMGGANTL YYIKNLDGKNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 077-3N19 (G2) (76) SMGGANTL YYIKNLDGKNKIENVVTLGGANRLTTSKALPGTDPNQKILYTSIYGSADMIVMNYLSKLDGAKNVQI
SEQ: 078-G2.2 (76) SMGGANTL YYIKNLDGKNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYGSADMIVMNYLSKLDGAKNVQI
SEQ: 079-2C3 (76) SMGGANTL YYIKNLDGKNKIENVVTIGGANGLVSSRALPGTDPNQKILYTSIYSSADLIVVNSLSRLIGARNVQI
SEQ: 080-2F11 (76) SMGGANTL YYIKNLDGKNKIENVVTLGGANRLTTSRALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 081-KV11 (6C7) (76) SMGGANTL YYIKNLDGKNKIENVVTLGGANRLTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 082-KV6 (3A1) (76) SMGGANTL YYIKNLDGKNKIENVVTLGGANRLTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 083-KV2 (2D1) (76) SMGGANTL YYIKNLDGKNKIENVVTLGGANRLTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 084-N2.5 (76) SMGGANTL YYIKNLDGKNKIENVVTLGGANRLTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 085-KV5 (2H6) (76) SMGGANTL YYIKNLDGKNKIENVVTLGGANRLVTGKALPGTDPNQKILYASVYSSADMIVMNYLSKLDGAKNVQI
SEQ: 086-3E5 (76) SMGGANTL YYIKNLDGKNKIENVVTLGGANRLTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 087-G2.1 (76) SMGGANTL YYIKNLDGKNKIENVVTLGGANRLTTSRALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 088-3H24 (G2) (76) SMGGANTL YYIKNLDGKNKIENVVTLGGANRLTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 089-KV10 (4G6) (76) SMGGANTL YYIKNLDGKNKVENVVTLGGANRLTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 090-KV12 (6D4) (76) SMGGANTL YYIKNLDGKNKVENVVTLGGANRLTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 091-N2.2 (76) SMGGANTL YYIKNLDGKNKVENVVTLGGANRLTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 092-N2.3 (76) SMGGANTL YYIKNLDGKNKVENVVTLGGANRLTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 093-N2.1 (76) SMGGANTL YYIKNLDGKNKVENVVTLGGANRLTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 094-KV4 (2E12) (76) SMGGANTL YYIKNLDGKNKIENVVTLGGANRLTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 095-KV9 (4C6) (76) SMGGANTL YYIKNLDGKNKIENVVTLGGANRLTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 096-7D6 (76) SMGGANTL YYIKNLDGKNKIENVVTLGGANRLTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 097-3F3 (76) SMGGANTL YYIKNLDGKNKIENVVTLGGANRLTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 098-2D11 (G2) (76) SMGGANTL YYIKNLDGKNKIENVVTLGGANRLTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 099-3C23 (G2) (76) SMGGANTL YYIKNLDGKNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 100-G2.3 (76) SMGGANTL YYIKNLDGKNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 101-2A3 (76) SMGGANTL YYIKNLDGKNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 102-2F4 (76) SMGGANTL YYIKNLDGKNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 103-2B9 (G2) (76) SMGGANTL YYIKNLDGKNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 104-2C5 (76) SMGGANTL YYIKNLDGKNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 105-KV1 (2A6) (76) SMGGANTL YYIKNLDGKNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 106-2D13 (G2) (76) SMGGANTL YYIKNLDGKNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 107-3C8 (76) SMGGANTL YYIKNLDGKNKVENVVTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI
SEQ: 108-2D5 (76) SMGGANTL YYIKNLDGKNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNVQI

Figure 6b

	151	180
SEQ: 075-1f15 (G2)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 076-3C12	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 077-3N19 (G2)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 078-G2.2	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 079-2C3	(151)	HGVGHIGLLTSSQVKGYIKEGLNGGGHNTN
SEQ: 080-2F11	(151)	HGVGHIGLLMNSQVKGYIKEGLNGGGLNTN
SEQ: 081-KV11 (6C7)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 082-KV6 (3A1)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 083-KV2 (2D1)	(151)	HGVGHIGLLYSSQVNSLIKEGLNGGQNTN
SEQ: 084-N2.5	(151)	HGVGHTGLMNSQVNSLIKEGLNGGGHNTN
SEQ: 085-KV5 (2H6)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 086-3E5	(151)	HGVGHIGLLYSSQVNSLIKEGLNGGGLNTN
SEQ: 087-G2.1	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 088-3H24 (G2)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 089-KV10 (4G6)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGHNTN
SEQ: 090-KV12 (6D4)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGHNTN
SEQ: 091-N2.2	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGHNTN
SEQ: 092-N2.3	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGHNTN
SEQ: 093-N2.1	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGHNTN
SEQ: 094-KV4 (2E12)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGHNTN
SEQ: 095-KV9 (4C6)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGHNTN
SEQ: 096-7D6	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 097-3F3	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGQNTN
SEQ: 098-2D11 (G2)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGQNTN
SEQ: 099-3C23 (G2)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGHNTN
SEQ: 100-G2.3	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGQNTN
SEQ: 101-2A3	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGGLNTN
SEQ: 102-2F4	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGQNTN
SEQ: 103-2B9 (G2)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGQNTN
SEQ: 104-2C5	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGQNTN
SEQ: 105-KV1 (2A6)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGQNTN
SEQ: 106-2D13 (G2)	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGQNTN
SEQ: 107-3C8	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGQNTN
SEQ: 108-2D5	(151)	HGVGHIGLLMNSQVNSLIKEGLNGGQNTN

Figure 6c